

**APPENDIX B**  
**MARKED-UP VERSION OF SUBSTITUTE SEQUENCE LISTING**  
**WITH MARKINGS TO SHOW CHANGES MADE**  
**(Application Serial No. 10/046,671)**

# SEQUENCE LISTING

<110> Boot, Hendrik J.  
 Huurne ter, Anna A.H.M  
 Peeters, Bernardus P.H.

<120> Mosaic Infectious Bursal Disease Virus Vaccines

<130> 2183-5238US

<140> US 10/046,671  
 <141> 2002-01-14

<150> PCT/NL00/00493  
 <151> 2000-07-13

<150> EP 99202316.8  
 <151> 1999-07-14

<160> 87

<170> PatentIn Ver. 2.1

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<400> 1  
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<220> <221> misc\_feature  
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<210> 6  
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<210> 7  
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21

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17

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accagccaa tcacatcc

18

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ctcaaagaag atggagacc

19

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24

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22

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21

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21

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 tatcattgat ggtcagtaga g 21  
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gtaaaacgac ggccagt 17

<210> 25  
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<220>  
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ccggcacagc tadcct 16

<210> 26  
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<220>  
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<223> Primer ANC2

<400> 26  
ctgcctgtcc tggagcc 17

<210> 27  
<211> 20  
<212> DNA  
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<220>  
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<223> Primer HY4P

<400> 27  
acataatccg ggccataagg 20

<210> 28  
<211> 17  
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<220>  
<221> misc\_feature  
<223> Primer ANC3

<400> 28  
cgatgggcgt tcgggtc 17



<210> 29  
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 <220>  
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 <223> Primer ANC5  
  
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 cccatctgga gcatatcc 18  
  
 <210> 30  
 <211> 18  
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 <220>  
 <221> misc\_feature  
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 <220>  
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 <222> (1)..(30)  
 <223> Anchor  
  
 <400> 31  
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 <211> 20  
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 <222> (1)..(20)  
 <223> Anchor primer  
  
 <400> 32  
 gaaggatcca gaatcgatag 20  
  
 <210> 33  
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<212> DNA  
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 <220>  
 <221> primer\_bind  
 <222> (1)..(19)  
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 ggggacccgc gaacggatc 19  
  
  
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 ggggacccgc gaacgg 16  
  
  
 <210> 35  
 <211> 47  
 <212> DNA  
 <213> Infectious bursal disease virus  
  
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 <221> primer\_bind  
 <222> (1)..(47)  
 <223> Primer T7AC0  
  
 <400> 35  
 ggaattctaa tacgactcac tataggatac gatcgggtctg accccgg 47  
  
  
 <210> 36  
 <211> 15  
 <212> DNA  
 <213> Infectious bursal disease virus  
  
 <220>  
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 <222> (1)..(15)  
 <223> Primer BNC1  
  
 <400> 36  
 gggggccccc gcagg 15  
  
  
 <210> 37

<211> 45  
 <212> DNA  
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 <220>  
 <221> primer\_bind  
 <222> (1)..(45)  
 <223> Primer T7BC1"  
  
 <400> 37  
 ggaattctaa tacgactcac tataggatac gatgggtctg accct 45  
  
 <210> 38  
 <211> 10  
 <212> RNA  
 <213> Infectious bursal disease virus  
  
 <220>  
 <221> misc\_RNA  
 <222> (1)..(10)  
 <223> 5'-Terminus of the A-segment coding strand  
           of IBDV  
  
 <400> 38  
 ugauacgauc 10  
  
 <210> 39  
 <211> 10  
 <212> RNA  
 <213> Infectious bursal disease virus  
  
 <220>  
 <221> misc\_RNA  
 <222> (1)..(10)  
 <223> 5'-Terminus of the A-segment coding strand  
           of IBDV  
  
 <400> 39  
 agauacgauc 10  
  
 <210> 40  
 <211> 10  
 <212> RNA  
 <213> Infectious bursal disease virus  
  
 <220>  
 <221> misc\_RNA  
 <222> (1)..(10)  
 <223> 5'-Terminus of the A-segment coding strand  
           of IBDV  
  
 <400> 40

ggauacgauc

10

<210> 41  
<211> 10  
<212> RNA  
<213> Infectious bursal disease virus  
  
<220>  
<221> misc\_RNA  
<222> (1)..(10)  
<223> Consensus sequence corresponding to the  
5'-terminus of the A-segment coding strand of  
IBDV

<400> 41  
ggauacgauc

10

<210> 42  
<211> 4  
<212> RNA  
<213> Infectious bursal disease virus

<220>  
<221> misc\_RNA  
<222> (1)..(4)  
<223> Complementary sequence of the 5'-terminus  
of the A-segment non-coding strand of IBDV

<400> 42  
cggg

4

<210> 43  
<211> 8  
<212> RNA  
<213> Infectious bursal disease virus

<220>  
<221> misc\_RNA  
<222> (1)..(8)  
<223> Complementary sequence of the 5'-terminus  
of the A-segment non-coding strand of IBDV

<400> 43  
cggguccc

8

<210> 44  
<211> 9  
<212> RNA  
<213> Infectious bursal disease virus

<220>

<221> misc\_RNA  
 <222> (1)..(9)  
 <223> Complementary sequence of the 5'-terminus  
 of the A-segment non-coding strand of IBDV

<400> 44  
 cgggucccu

9

<210> 45  
 <211> 9  
 <212> RNA  
 <213> Infectious bursal disease virus

<220>  
 <221> misc\_RNA  
 <222> (1)..(9)  
 <223> Complementary sequence of the 5'-terminus  
 of the A-segment non-coding strand of IBDV

<400> 45  
 cgggucccc

9

<210> 46  
 <211> 11  
 <212> RNA  
 <213> Infectious bursal disease virus

<220>  
 <221> misc\_RNA  
 <222> (1)..(11)  
 <223> Complementary sequence of the 5'-terminus  
 of the A-segment non-coding strand of IBDV

<400> 46  
 cggguccccc c

11

<210> 47  
 <211> 12  
 <212> RNA  
 <213> Infectious bursal disease virus

<220>  
 <221> misc\_RNA  
 <222> (1)..(12)  
 <223> Complementary sequence of the 5'-terminus  
 of the A-segment non-coding strand of IBDV

<400> 47  
 cggguccccc cu

12

<210> 48

<211> 12  
<212> RNA  
<213> Infectious bursal disease virus

<220>  
<221> misc\_RNA  
<222> (1)..(12)  
<223> Complementary sequence of the 5'-terminus  
of the A-segment non-coding strand of IBDV

<400> 48  
cggguccccc cc

12

<210> 49  
<211> 9  
<212> RNA  
<213> Infectious bursal disease virus

<220>  
<221> misc\_RNA  
<222> (1)..(9)  
<223> Consensus complementary sequence of the  
5'-terminus of the A-segment non-coding strand of  
IBDV

<400> 49  
cgggucccc

9

<210> 50  
<211> 10  
<212> RNA  
<213> Infectious bursal disease virus

<220>  
<221> misc\_RNA  
<222> (1)..(10)  
<223> 5'-Terminus of the B-segment coding strand  
of IBDV

<400> 50  
ugauacgaug

10

<210> 51  
<211> 10  
<212> RNA  
<213> Infectious bursal disease virus

<220>  
<221> misc\_RNA  
<222> (1)..(10)  
<223> 5'-Terminus of the B-segment coding strand  
of IBDV

<400> 51  
ggauacgaug 10

<210> 52  
<211> 10  
<212> RNA  
<213> Infectious bursal disease virus

<220>  
<221> misc\_RNA  
<222> (1)..(10)  
<223> Consensus sequence of the 5'-terminus of  
the B-segment coding strand of IBDV

<400> 52  
ggauacgaug 10

<210> 53  
<211> 8  
<212> RNA  
<213> Infectious bursal disease virus

<220>  
<221> misc\_RNA  
<222> (1)..(8)  
<223> Complementary sequence of the 5'-terminus  
of the B-segment non-coding strand of IBDV

<400> 53  
gggggcca. 78

<210> 54  
<211> 8  
<212> RNA  
<213> Infectious bursal disease virus

<220>  
<221> misc\_RNA  
<222> (1)..(8)  
<223> Complementary sequence of the 5'-terminus  
of the B-segment non-coding strand of IBDV

<400> 54  
gggggccu 8

<210> 55  
<211> 8  
<212> RNA  
<213> Infectious bursal disease virus

<220>

<221> misc\_RNA  
<222> (1)..(8)  
<223> Complementary sequence of the 5'-terminus  
of the B-segment non-coding strand of IBDV

<400> 55  
ggggggccc

8

<210> 56  
<211> 9  
<212> RNA  
<213> Infectious bursal disease virus

<220>  
<221> misc\_RNA  
<222> (1)..(9)  
<223> Complementary sequence of the 5'-terminus  
of the B-segment non-coding strand of IBDV

<400> 56  
ggggggcccc

9

<210> 57  
<211> 10  
<212> RNA  
<213> Infectious bursal disease virus

<220>  
<221> misc\_RNA  
<222> (1)..(10)  
<223> Complementary sequence of the 5'-terminus  
of the B-segment non-coding strand of IBDV

<400> 57  
gguggccccc

10

<210> 58  
<211> 11  
<212> RNA  
<213> Infectious bursal disease virus

<220>  
<221> misc\_RNA  
<222> (1)..(11)  
<223> Complementary sequence of the 5'-terminus  
of the B-segment non-coding strand of IBDV

<400> 58  
gggggcccc c

11

<210> 59



<211> 11  
 <212> RNA  
 <213> Infectious bursal disease virus  
  
 <220>  
 <221> misc\_RNA  
 <222> (1)..(11)  
 <223> Complementary sequence of the 5'-terminus  
           of the B-segment non-coding strand of IBDV  
  
 <400> 59  
 gggggccccc g

11

<210> 60  
 <211> 10  
 <212> DNA  
 <213> Infectious bursal disease virus  
  
 <220>  
 <221> misc\_RNA  
 <222> (1)..(10)  
 <223> Consensus complementary sequence of the  
           5'-terminus of the B-segment non-coding strand of  
           IBDV  
  
 <400> 60  
 gggggccccc

10

<210> 61  
 <211> 119  
 <212> PRT  
 <213> Infectious bursal disease virus  
  
 <220>  
 <221> DOMAIN  
 <222> (1)..(119)  
 <223> Amino acid sequence of the hypervariable  
           region of VP2 of IBDV isolates D6948, rD6948, UK661  
           5123, 96-C6, 97-B4, 97-B5, 97-B6, Hungary, OKYM,  
           TKSM and HK46

<400> 61  
 Ala Ala Asp Asp Tyr Gln Phe Ser Ser Gln Tyr Gln Ala Gly Gly Val  
   1                  5                  10                  15  
  
 Thr Ile Thr Leu Phe Ser Ala Asn Ile Asp Ala Ile Thr Ser Leu Ser  
           20                  25                  30  
  
 Ile Gly Gly Glu Leu Val Phe Gln Thr Ser Val Gln Gly Leu Ile Leu  
           35                  40                  45  
  
 Gly Ala Thr Ile Tyr Leu Ile Gly Phe Asp Gly Thr Ala Val Ile Thr  
   50                  55                  60

Arg Ala Val Ala Ala Asp Asn Gly Leu Thr Ala Gly Thr Asp Asn Leu  
65 70 75 80

Met Pro Phe Asn Ile Val Ile Pro Thr Ser Glu Ile Thr Gln Pro Ile  
85 90 95

Thr Ser Ile Lys Leu Glu Ile Val Thr Ser Lys Ser Gly Gly Gln Ala  
100 105 110

Gly Asp Gln Met Ser Trp Ser  
115

<210> 62  
<211> 119  
<212> PRT  
<213> Infectious bursal disease virus

<220>  
<221> DOMAIN  
<222> (1)..(119)  
<223> Amino acid sequence of the hypervariable  
region of VP2 of IBDV isolate 96-B4

<400> 62  
Ala Ala Asp Asp Tyr Gln Phe Ser Ser Gln Tyr Gln Pro Gly Gly Val  
1 5 10 15

Thr Ile Thr Leu Phe Ser Ala Asn Ile Asp Ala Ile Thr Ser Leu Ser  
20 25 30

Val Gly Gly Glu Leu Val Phe Gln Thr Ser Val Gln Gly Leu Val Leu  
35 40 45

Gly Ala Thr Ile Tyr Leu Ile Gly Phe Asp Gly Thr Thr Val Ile Thr  
50 55 60

Arg Ala Val Ala Ala Asn Asn Gly Leu Thr Thr Gly Thr Asp Asn Leu  
65 70 75 80

Leu Pro Phe Asn Ile Val Ile Pro Thr Asn Glu Ile Thr Gln Pro Ile  
85 90 95

Thr Ser Ile Lys Leu Glu Ile Val Thr Ser Lys Ser Gly Gly Gln Ala  
100 105 110

Gly Asp Gln Met Ser Trp Ser  
115

<210> 63  
<211> 119  
<212> PRT  
<213> Infectious bursal disease virus

<220>  
 <221> DOMAIN  
 <222> (1)..(119)  
 <223> Amino acid sequence of the hypervariable  
 region of VP2 of IBDV isolate 96-C4

<400> 63  
 Ala Ala Asp Asp Tyr Gln Phe Ser Ser Gln Tyr Gln Leu Gly Gly Val  
 1 5 10 15  
 Thr Ile Thr Leu Phe Ser Ala Asn Ile Asp Ala Ile Thr Ser Leu Ser  
 20 25 30  
 Ile Gly Gly Glu Leu Val Phe Asn Thr Ser Val Gln Gly Leu Ala Leu  
 35 40 45  
 Asn Ala Thr Ile Tyr Leu Ile Gly Phe Asp Gly Thr Thr Val Ile Thr  
 50 55 60  
 Arg Ala Val Ala Ser Asp Asn Gly Leu Thr Thr Gly Ile Asp Asn Leu  
 65 70 75 80  
 Met Pro Phe Asn Ile Val Ile Pro Thr Asn Glu Ile Thr Gln Pro Ile  
 85 90 95  
 Thr Ser Ile Lys Leu Glu Ile Val Thr Ser Lys Ser Gly Gly Gln Ala  
 100 105 110  
 Gly Asp Gln Met Ser Trp Ser  
 115

<210> 64  
 <211> 119  
 <212> PRT  
 <213> Infectious bursal disease virus

<220>  
 <221> DOMAIN  
 <222> (1)..(119)  
 <223> Amino acid sequence of the hypervariable  
 region of VP2 of a IBDV isolate 96-C5

<400> 64  
 Ala Ala Asp Asp Tyr Gln Phe Ser Ser Gln Tyr Gln Pro Gly Gly Val  
 1 5 10 15  
 Thr Ile Thr Leu Phe Ser Ala Asn Ile Asp Ala Ile Thr Ser Leu Ser  
 20 25 30  
 Val Gly Gly Glu Leu Val Phe Gln Thr Ser Val Gln Gly Leu Val Leu  
 35 40 45  
 Gly Ala Thr Ile Tyr Leu Ile Gly Phe Asp Gly Thr Ala Val Ile Thr

50                                      55                                      60  
 Arg Ala Val Ala Ala Tyr Asn Gly Leu Thr Thr Gly Thr Asp Asn Leu  
 65                                      70                                      75                                      80  
 Leu Pro Phe Asn Ile Val Ile Pro Thr Asn Glu Ile Thr Gln Pro Ile  
                                     85                                      90                                      95  
 Thr Ser Ile Lys Leu Glu Ile Val Thr Ser Lys Ser Gly Gly Gln Ala  
                                     100                                      105                                      110  
 Gly Asp Gln Met Ser Trp Ser  
                                     115

<210> 65  
 <211> 119  
 <212> PRT  
 <213> Infectious bursal disease virus

<220>  
 <221> DOMAIN  
 <222> (1)..(119)  
 <223> Amino acid sequence of the hypervariable  
                                     region of VP2 of IBDV isolate 97-B3

<400> 65  
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   1                                      5                                      10                                      15  
 Thr Ile Thr Leu Phe Ser Ala Asn Ile Asp Ala Ile Thr Ser Leu Ser  
                                     20                                      25                                      30  
 Ile Gly Gly Glu Leu Val Phe Gln Thr Ser Val Gln Gly Leu Ile Leu  
                                     35                                      40                                      45  
 Gly Ala Thr Ile Tyr Leu Ile Gly Phe Asp Gly Thr Ala Val Ile Thr  
   50                                      55                                      60  
 Arg Ala Val Ala Ala Asn Asn Gly Leu Thr Ala Gly Thr Asp Asn Leu  
   65                                      70                                      75                                      80  
 Met Pro Phe Asn Ile Val Ile Pro Thr Ser Glu Ile Thr Gln Pro Ile  
                                     85                                      90                                      95  
 Thr Ser Ile Lys Leu Glu Ile Val Thr Ser Lys Ser Gly Gly Gln Ala  
                                     100                                      105                                      110  
 Gly Asp Gln Met Ser Trp Ser  
                                     115

<210> 66  
 <211> 119  
 <212> PRT

<213> Infectious bursal disease virus

<220>

<221> DOMAIN

<222> (1)..(119)

<223> Amino acid sequence of the hypervariable  
region of VP2 of IBDV isolate Zoontjes

<400> 66

Ala Ala Asp Asp Tyr Gln Phe Ser Ser Gln Tyr Gln Ala Gly Gly Val  
1 5 10 15

Thr Ile Thr Leu Phe Ser Ala Asn Ile Asp Ala Ile Thr Ser Leu Ser  
20 25 30

Ile Gly Gly Glu Leu Val Phe Gln Thr Ser Val Gln Gly Leu Ile Leu  
35 40 45

Gly Ala Thr Ile Tyr Leu Ile Gly Phe Asp Gly Thr Ala Val Ile Thr  
50 55 60

Arg Ala Val Ala Ala Asp Asn Gly Leu Thr Ala Gly Thr Asp Asn Leu  
65 70 75 80

Met Pro Phe Asn Ile Val Ile Pro Thr Ser Glu Thr Thr Gln Pro Ile  
85 90 95

Thr Ser Ile Lys Leu Val Ile Val Thr Ser Lys Ser Gly Gly Gln Ala  
100 105 110

Gly Asp Gln Met Ser Trp Ser  
115

<210> 67

<211> 119

<212> PRT

<213> Infectious bursal disease virus

<220>

<221> DOMAIN

<222> (1)..(119)

<223> Amino acid sequence of the hypervariable  
region of VP2 of IBDV isolate OKYMT

<400> 67

Ala Ala Asp Asp Tyr Gln Phe Ser Ser Gln Tyr Gln Ala Gly Gly Val  
1 5 10 15

Thr Ile Thr Leu Phe Ser Ala Asn Ile Asp Ala Ile Thr Ser Leu Ser  
20 25 30

Ile Gly Gly Glu Leu Val Phe Gln Thr Ser Val Gln Gly Leu Thr Leu  
35 40 45

Gly Ala Thr Ile Tyr Leu Ile Gly Phe Asp Gly Thr Ala Val Ile Thr  
 50 55 60  
 Arg Ala Val Ala Ala Asn Asn Gly Leu Thr Thr Gly Thr Asp Asn Leu  
 65 70 75 80  
 Met Pro Phe Asn Ile Val Ile Pro Thr Ser Glu Ile Thr Gln Pro Ile  
 85 90 95  
 Thr Ser Ile Lys Leu Glu Ile Val Thr Phe Lys Ser Gly Gly Gln Ala  
 100 105 110  
 Gly Asp Gln Met Ser Trp Ser  
 115

<210> 68  
 <211> 119  
 <212> PRT  
 <213> Infectious bursal disease virus

<220>  
 <221> DOMAIN  
 <222> (1)..(119)  
 <223> Amino acid sequence of the hypervariable  
 region of VP2 of IBDV isolate TKSMT

<400> 68  
 Ala Ala Asp Asp Tyr Gln Phe Ser Ser Gln Tyr Gln Ala Gly Gly Val  
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 Thr Ile Thr Leu Phe Ser Ala Asn Ile Asp Ala Ile Thr Ser Leu Ser  
 20 25 30  
 Ile Gly Gly Glu Leu Val Phe His Thr Ser Val Gln Gly Leu Ile Leu  
 35 40 45  
 Asp Ala Thr Ile Tyr Leu Ile Gly Phe Asp Gly Thr Ala Val Thr Thr  
 50 55 60  
 Arg Ala Val Ala Ala Asn Asn Gly Leu Thr Thr Gly Thr Asp Asn Leu  
 65 70 75 80  
 Met Pro Phe Asn Ile Val Ile Pro Thr Ser Glu Ile Thr Gln Pro Ile  
 85 90 95  
 Thr Ser Ile Lys Leu Glu Ile Val Thr Ser Lys Ser Gly Gly Gln Ala  
 100 105 110  
 Gly Asp Gln Met Ser Trp Ser  
 115

<210> 69  
 <211> 119

<212> PRT  
 <213> Infectious bursal disease virus

<220>  
 <221> DOMAIN  
 <222> (1)..(119)  
 <223> Amino acid sequence of the hypervariable  
 region of VP2 of IBDV isolate HK46-NT

<400> 69  
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             20                    25                    30  
 Ile Gly Gly Glu Leu Val Phe Gln Thr Ser Val Gln Gly Leu Ile Leu  
             35                    40                    45  
 Gly Ala Thr Ile Tyr Leu Ile Gly Phe Asp Gly Thr Ala Val Ile Thr  
             50                    55                    60  
 Arg Ala Val Ala Ala Asn Asn Gly Leu Thr Thr Gly Thr Asp Asn Leu  
             65                    70                    75                    80  
 Met Pro Phe Asn Ile Val Ile Pro Thr Ser Glu Ile Thr Gln Pro Ile  
                     85                    90                    95  
 Thr Ser Ile Lys Leu Glu Ile Val Thr Ser Lys Ser Gly Gly Gln Ala  
             100                    105                    110  
 Gly Asp Gln Met Ser Trp Ser  
             115

<210> 70  
 <211> 3260  
 <212> DNA  
 <213> Infectious bursal disease virus

<220>  
 <221> misc\_feature  
 <222> (1)..(3260)  
 <223> Consensus cDNA sequence of IBDV A-segment

<400> 70  
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 gatcgacgag atgacraacc tgcaagatca aacccaacag attgttccgt tcatacggag 180  
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 ctactgcagg ctagtgagtc ggagtctcac agtgaggtca agcacactyc ctggtggcgt 480  
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<210> 71
<211> 3260
<212> DNA
<213> Infectious bursal disease virus

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<220>
<221> misc_feature

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<222> (1)..(3260)

<223> cDNA sequence CEF94-A of IBV A-segment

<400> 71

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<210> 72

<211> 3260

<212> DNA

<213> Infectious bursal disease virus

<220>

<221> misc\_feature

<222> (1)..(3260)

<223> cDNA sequence D6948-A of IBDV A-segment

<400> 72

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<210> 73

<211> 964

<212> DNA

<213> Infectious bursal disease virus

<220>

<221> misc\_feature

<222> (1)..(964)

<223> cDNA sequence TY89-A of IBV A-segment

<400> 73

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<210> 74

<211> 2827

<212> DNA

<213> Infectious bursal disease virus

<220>

<221> misc\_feature  
 <222> (1)..(2827)  
 <223> Consensus cDNA sequence of IBV B-segment

<400> 74

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caggag tact tcccwa arta ctaccca aca caycgcc cka gcaagg araa gcccaat gcg 480
taccgc ccmg ayatcg cayt actcaag cag atgaty tacy tgtttct cca ggttcc mgag 540
gccamm gahr rcctwa arga tgargtm acc ctmytra ccc aaaacat wag rgayaarg cc 600
taygg ragtg ggacct acat gggacarg cm acymgact tg tkgyat gaa rgaggy gcc 660
actggr agaa acccaa acaa rgatcct cta aagctt gggg acacyttt ga gagcat mgcs 720
cagctact tg acatcac wyt accggt aggc ccaccc ggtg aggatg acaa gccctg ggt 780
ccactc aca grgtgcc gtc amggat gttg gtwtg acgg gmgacg taga tggsgam ttt 840
gaggttg arg aytacctt cc caaaat caat ctaagtc at caagtg gact rccmtat gtw 900
ggtcgc acca aaggag arac wattggs gag atgatag cya tmtcra acca gtttct ymga 960
gagctat car crctgyt gaa gcarggt gca gggacaa arg ggtcra acaa gaagaag ctr 1020
ctcagc atgy taagt gacta ytggta ctta tcatgy gggc ttttg tttcc maaggct gar 1080
aggtac gaca aaagyac atg gctcac caag acccgk aaca tatggtc agc tccatcm cca 1140
acacac ctca tgatct cwat gatmac ctgg cccgtg atgt ccaayag ccc aaayaac gtg 1200
ttgaac attg argggt gtcc rtcact ctac aarttca acc cgttyag agg wgggyt raac 1260
aggatc gts agtgga twt ggcycgg gaw gaacca aagg cyytwgt ata tgckgaca ac 1320
atatac attg tycactc maa cacgtg gtac tcaatt gacc tagaga aggg tgaggc aaac 1380
tg cackc gyc aacacat gca rgccgc matg tactac atmc tyaccag agg rtggctm gay 1440
aacggy gacc cmatgtt caa tcarac atgg gccacctt tg csatga acat tgcccc wgt 1500
ctagtk gtg actcat crt g yctgat watg aacctk cara tyaagac mta tggtc aaggc 1560
agyggga atg cagccac stt catcaaca ac cayctyyt ka gcacsct wgt gctwg accag 1620
tggaacyt ga tgarrcar cc yagwcc agac agcgarg agt tcaart caat tgargaca ag 1680
ctr ggyat ca acttya agat tgagagg tcc attgat gaya tyagggg caa gctsag acag 1740
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ccaactg twt agctkg acct actm ggrtgg tcwgcwac wt acagcaaa aga tctyggg gatc 1860
tatgtgc cgg tgcttg acaa ggaacgc yta ttttgyt ctg ctgctat cc caarggr gta 1920
gagaaya ara gyctca artc caargty ggg atcgagc arg cataca argt wgtcagg tay 1980
gaggcg ttga ggttggt agg tggttg gaac taccact cc tgaacaa agc ytgcaaga ay 2040
aaygcarg yg cmgctc ggcg gcatct ggag gccaa ggggt tcccrct cga ygagtt cctm 2100
gccgag tgg cwgagy tgtc mgagt tccgw gargcyt tccg aaggctt caa yatcaag ctg 2160
acmgta acay ckgagag cct mgccga actk aacarr ccag taccctcc caa rccyccaa at 2220
gtcaac agac cagtca acac yggk ggrctm aaggc agtca gcaaygc ct caagacc ggy 2280
cggtayagra aygaag ccgg actragt ggy ctgctc ctyc tagccac mgc mmgmag ccgw 2340
ctrcarg ayg cagtya aggc caaggc agar gccgagaa ac tccaca agtc yaagccm gay 2400
gaccccg atg cagact ggtt ygaamgrt ca gaaacyt gt cagacct ket ggagaa agcc 2460
gacaty gcca gcaaggtc gc ycactc agca ctgctg gaaa caagcg acgc ycttga agcr 2520
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gccgtg aaaa tggccaa amg gcggca acgc caaaarg aga gccgcca aya gccatgat gg 2760
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ggcccc 2827

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<210> 75  
 <211> 2827  
 <212> DNA  
 <213> Infectious bursal disease virus  
  
 <220>  
 <221> misc\_feature  
 <222> (1)..(2827)  
 <223> cDNA sequence CEF94-B of IBDV B-segment

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 cttgccagcc ctagtcgact ggcaaagttc ctccagagaga acggctacaa agttytgacg 300  
 ccacggtctc tgcccagaaa tgaggagtat gagaccgacc aaataactccc agacttagca 360  
 tggatgacgac agatagaagg ggctgtttta aaacccactc tatctctccc tattggagat 420  
 caggagtact tcccaaagta ctacccaaca catcgcccta gcaaggagaa gcccaatgag 480  
 taccgcccag acatcgact actcaagcag atgatttacc tgtttctcca ggttccagag 540  
 gccaacgagg gcctaaagga tgaagtaacc ctcttgaccc aaaacataag ggacaaggcc 600  
 tatggaagtg ggacctacat gggacaagca actcgacttg tggccatgaa ggaggtcgcc 660  
 actggaagaa acccaacaaa ggatcctcta aagcttgggt acacttttga gagcatcgcg 720  
 cagctacttg acatcacact accggtaggc ccacccggtg aggatgacaa gccctgggtg 780  
 ccactcacia gagtgccgtc accgatgttg gtactgacgg gagacgtaga tggcgacttt 840  
 gaggttgaag attaccttcc caaaatcaac ctcaagtcac caagtggact accatatgta 900  
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 gagctatcaa cactgttgaa gcaagggtgca gggacaaagg ggtcaaacia gaagaagcta 1020  
 ctcagcatgt taagtgacta ttggtactta tcatgcgggc ttttgtttcc aaaggctgaa 1080  
 aggtacgaca aaagtacatg gctcaccaag acccggaaca tatggtcagc tccatcccca 1140  
 acacacctca tgatctctat gatcacctgg cccgtgatgt ccaacagccc aaataacgtg 1200  
 ttgaacattg aagggtgtcc atcaactctac aaattcaacc cgttcagagg aggggtgaac 1260  
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 tgcactcgcc aacacatgca agccgcaatg tactacatac tcaccagagg gtggtcagac 1440  
 aacggcgacc caatgttcaa tcaaacatgg gccaccttgg ccatgaacat tgcccctgct 1500  
 ctagtggtag actcatcgtg cctgataatg aacctgcaaa ttaagacctg tgggtcaaggc 1560  
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 gtcaacagac cagtcaacac tgggggactc aaggcagtc gcaacgcct caagaccgtg 2280  
 cggtagacga acgaagccgg actgagtggt ctgctccttc tagccacagc aagaagccgt 2340  
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 gaccccgatg cagactgggt cgaaagatca gaaactctgt cagaccttct ggagaaagcc 2460  
 gacatcgcca gcaaggctgc cactcagca ctggtggaac caagcgacgc ccttgaagca 2520  
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 tccaaccccg ttgttgggct ccacctgccc gccaaagag ccaccgggtg ccaggccgct 2640

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cttctcggag caggaacgag cagaccaatg gggatggagg cccaacacg gtccaagaac 2700
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<210> 76
<211> 2827
<212> DNA
<213> Infectious bursal disease virus

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<220>
<221> misc_feature
<222> (1)..(2827)
<223> cDNA sequence D6948-B of IBV B-segment

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gttttcaata gtccacaggc gcgaagcaag atatcagcag cgttcggcat aaagcctaca 180
gctggacagg atgtggaaga actcctgata cctaaggctt ggggtgccacc tgaggatccc 240
ttggccagcc ctatgcgtct ggccaagttc ctcagggaaa acggctacaa gattctgcag 300
ccacggtctc tacctgagaa tgaggagtat gagaccgatc aaatactccc tgacctagct 360
tggtatgaggc agatagaggg agctgtttta aaaccaaccc tatctctccc cattggagac 420
caggagtact tccctaaata ctaccaaca caccgcccga gcaaggaaaa gcccaatgcg 480
taccgccccg atatcgcatc actcaagcag atgatctact tgtttctcca ggttcccag 540
gccacagata acctaaaga tgaggtcacc ctactaaccc aaaacattag agataaagcc 600
tacgggagtg ggacctacat gggacaggcc accagacttg ttgctatgaa agagggtgcc 660
actgggagaa acccaaaca agatcctcta aagcttgggt acacctttga gagcatagcc 720
cagctacttg acatcacttt accggtaggc ccaccgggtg aggatgacaa gccctgggta 780
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cggtatagaa atgaagccgg actaagtggc ctcgtcctcc tagccaccgc ccgcagccga 2340
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ggcccc
2827

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<210> 77
<211> 1012
<212> PRT
<213> Infectious bursal disease virus

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<220>
<221> DOMAIN
<222> (1)..(1012)
<223> Consensus sequence of IBV polyprotein, whereby the Xaa
indicator may be any amino acid

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<220>
<221> MISC FEATURE
<222> (222)
<223> The 'Xaa' at position 222 may be any amino acid

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<220>
<221> MISC FEATURE
<222> (242)
<223> The 'Xaa' at position 242 may be any amino acid

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<220>
<221> MISC FEATURE
<222> (253)
<223> The 'Xaa' at position 253 may be any amino acid

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<220>
<221> MISC FEATURE
<222> (256)
<223> The 'Xaa' at position 256 may be any amino acid

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<220>
<221> MISC FEATURE
<222> (279)
<223> The 'Xaa' at position 279 may be any amino acid

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<220>
<221> MISC FEATURE
<222> (284)
<223> The 'Xaa' at position 284 may be any amino acid

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<220>

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<221> MISC FEATURE  
<222> (290)  
<223> The 'Xaa' at position 290 may be any amino acid

<220>  
<221> MISC FEATURE  
<222> (294)  
<223> The 'Xaa' at position 294 may be any amino acid

<220>  
<221> MISC FEATURE  
<222> (299)  
<223> The 'Xaa' at position 299 may be any amino acid

<220>  
<221> MISC FEATURE  
<222> (330)  
<223> The 'Xaa' at position 330 may be any amino acid

<220>  
<221> MISC FEATURE  
<222> (451)  
<223> The 'Xaa' at position 451 may be any amino acid

<220>  
<221> MISC FEATURE  
<222> (541)  
<223> The 'Xaa' at position 541 may be any amino acid

<220>  
<221> MISC FEATURE  
<222> (680)  
<223> The 'Xaa' at position 680 may be any amino acid

<220>  
<221> MISC FEATURE  
<222> (685)  
<223> The 'Xaa' at position 685 may be any amino acid

<220>  
<221> MISC FEATURE  
<222> (715)  
<223> The 'Xaa' at position 715 may be any amino acid

<400> 77  
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Ser Leu Leu Met Pro Thr Thr Gly Pro Ala Ser Ile Pro Asp Asp Thr  
20 25 30  
Leu Glu Lys His Thr Leu Arg Ser Glu Thr Ser Thr Tyr Asn Leu Thr  
35 40 45  
Val Gly Asp Thr Gly Ser Gly Leu Ile Val Phe Phe Pro Gly Phe Pro



50		55		60
Gly Ser Ile Val Gly Ala His Tyr Thr Leu Gln Ser Asn Gly Asn Tyr				
65		70		75
Lys Phe Asp Gln Met Leu Leu Thr Ala Gln Asn Leu Pro Ala Ser Tyr				
	85		90	95
Asn Tyr Cys Arg Leu Val Ser Arg Ser Leu Thr Val Arg Ser Ser Thr				
	100		105	110
Leu Pro Gly Gly Val Tyr Ala Leu Asn Gly Thr Ile Asn Ala Val Thr				
	115		120	125
Phe Gln Gly Ser Leu Ser Glu Leu Thr Asp Val Ser Tyr Asn Gly Leu				
	130		135	140
Met Ser Ala Thr Ala Asn Ile Asn Asp Lys Ile Gly Asn Val Leu Val				
145		150		155
Gly Glu Gly Val Thr Val Leu Ser Leu Pro Thr Ser Tyr Asp Leu Gly				
	165		170	175
Tyr Val Arg Leu Gly Asp Pro Ile Pro Ala Ile Gly Leu Asp Pro Lys				
	180		185	190
Met Val Ala Thr Cys Asp Ser Ser Asp Arg Pro Arg Val Tyr Thr Ile				
	195		200	205
Thr Ala Ala Asp Asp Tyr Gln Phe Ser Ser Gln Tyr Gln Xaa Gly Gly				
	210		215	220
Val Thr Ile Thr Leu Phe Ser Ala Asn Ile Asp Ala Ile Thr Ser Leu				
225		230		235
Ser Xaa Gly Gly Glu Leu Val Phe Gln Thr Ser Val Xaa Gly Leu Xaa				
	245		250	255
Leu Gly Ala Thr Ile Tyr Leu Ile Gly Phe Asp Gly Thr Ala Val Ile				
	260		265	270
Thr Arg Ala Val Ala Ala Xaa Asn Gly Leu Thr Xaa Gly Thr Asp Asn				
	275		280	285
Leu Xaa Pro Phe Asn Xaa Val Ile Pro Thr Xaa Glu Ile Thr Gln Pro				
	290		295	300
Ile Thr Ser Ile Lys Leu Glu Ile Val Thr Ser Lys Ser Gly Gly Gln				
305		310		315
Ala Gly Asp Gln Met Ser Trp Ser Ala Xaa Gly Ser Leu Ala Val Thr				
	325		330	335
Ile His Gly Gly Asn Tyr Pro Gly Ala Leu Arg Pro Val Thr Leu Val				
	340		345	350

Ala Tyr Glu Arg Val Ala Thr Gly Ser Val Val Thr Val Ala Gly Val  
 355 360 365  
 Ser Asn Phe Glu Leu Ile Pro Asn Pro Glu Leu Ala Lys Asn Leu Val  
 370 375 380  
 Thr Glu Tyr Gly Arg Phe Asp Pro Gly Ala Met Asn Tyr Thr Lys Leu  
 385 390 395 400  
 Ile Leu Ser Glu Arg Asp Arg Leu Gly Ile Lys Thr Val Trp Pro Thr  
 405 410 415  
 Arg Glu Tyr Thr Asp Phe Arg Glu Tyr Phe Met Glu Val Ala Asp Leu  
 420 425 430  
 Asn Ser Pro Leu Lys Ile Ala Gly Ala Phe Gly Phe Lys Asp Ile Ile  
 435 440 445  
 Arg Ala Xaa Arg Arg Ile Ala Val Pro Val Val Ser Thr Leu Phe Pro  
 450 455 460  
 Pro Ala Ala Pro Leu Ala His Ala Ile Gly Glu Gly Val Asp Tyr Leu  
 465 470 475 480  
 Leu Gly Asp Glu Ala Gln Ala Ala Ser Gly Thr Ala Arg Ala Ala Ser  
 485 490 495  
 Gly Lys Ala Arg Ala Ala Ser Gly Arg Ile Arg Gln Leu Thr Leu Ala  
 500 505 510  
 Ala Asp Lys Gly Tyr Glu Val Val Ala Asn Leu Phe Gln Val Pro Gln  
 515 520 525  
 Asn Pro Val Val Asp Gly Ile Leu Ala Ser Pro Gly Xaa Leu Arg Gly  
 530 535 540  
 Ala His Asn Leu Asp Cys Val Leu Arg Glu Gly Ala Thr Leu Phe Pro  
 545 550 555 560  
 Val Val Ile Thr Thr Val Glu Asp Ala Met Thr Pro Lys Ala Leu Asn  
 565 570 575  
 Ser Lys Met Phe Ala Val Ile Glu Gly Val Arg Glu Asp Leu Gln Pro  
 580 585 590  
 Pro Ser Gln Arg Gly Ser Phe Ile Arg Thr Leu Ser Gly His Arg Val  
 595 600 605  
 Tyr Gly Tyr Ala Pro Asp Gly Val Leu Pro Leu Glu Thr Gly Arg Asp  
 610 615 620  
 Tyr Thr Val Val Pro Ile Asp Asp Val Trp Asp Asp Ser Ile Met Leu  
 625 630 635 640

Ser Lys Asp Pro Ile Pro Pro Ile Val Gly Asn Ser Gly Asn Leu Ala  
 645 650 655  
 Ile Ala Tyr Met Asp Val Phe Arg Pro Lys Val Pro Ile His Val Ala  
 660 665 670  
 Met Thr Gly Ala Leu Asn Ala Xaa Gly Glu Ile Glu Xaa Val Ser Phe  
 675 680 685  
 Arg Ser Thr Lys Leu Ala Thr Ala His Arg Leu Gly Leu Lys Leu Ala  
 690 695 700  
 Gly Pro Gly Ala Phe Asp Val Asn Thr Gly Xaa Asn Trp Ala Thr Phe  
 705 710 715 720  
 Ile Lys Arg Phe Pro His Asn Pro Arg Asp Trp Asp Arg Leu Pro Tyr  
 725 730 735  
 Leu Asn Leu Pro Tyr Leu Pro Pro Asn Ala Gly Arg Gln Tyr His Leu  
 740 745 750  
 Ala Met Ala Ala Ser Glu Phe Lys Glu Thr Pro Glu Leu Glu Ser Ala  
 755 760 765  
 Val Arg Ala Met Glu Ala Ala Ala Asn Val Asp Pro Leu Phe Gln Ser  
 770 775 780  
 Ala Leu Ser Val Phe Met Trp Leu Glu Glu Asn Gly Ile Val Thr Asp  
 785 790 795 800  
 Met Ala Asn Phe Ala Leu Ser Asp Pro Asn Ala His Arg Met Arg Asn  
 805 810 815  
 Phe Leu Ala Asn Ala Pro Gln Ala Gly Ser Lys Ser Gln Arg Ala Lys  
 820 825 830  
 Tyr Gly Thr Ala Gly Tyr Gly Val Glu Ala Arg Gly Pro Thr Pro Glu  
 835 840 845  
 Glu Ala Gln Arg Glu Lys Asp Thr Arg Ile Ser Lys Lys Met Glu Thr  
 850 855 860  
 Met Gly Ile Tyr Phe Ala Thr Pro Glu Trp Val Ala Leu Asn Gly His  
 865 870 875 880  
 Arg Gly Pro Ser Pro Gly Gln Leu Lys Tyr Trp Gln Asn Thr Arg Glu  
 885 890 895  
 Ile Pro Asp Pro Asn Glu Asp Tyr Leu Asp Tyr Val His Ala Glu Lys  
 900 905 910  
 Ser Arg Leu Ala Ser Glu Glu Gln Ile Leu Arg Ala Ala Thr Ser Ile  
 915 920 925  
 Tyr Gly Ala Pro Gly Gln Ala Glu Pro Pro Gln Ala Phe Ile Asp Glu

930                      935                      940  
 Val Ala Lys Val Tyr Glu Ile Asn His Gly Arg Gly Pro Asn Gln Glu  
 945                      950                      955                      960  
 Gln Met Lys Asp Leu Leu Leu Thr Ala Met Glu Met Lys His Arg Asn  
                     965                      970                      975  
 Pro Arg Arg Ala Pro Pro Lys Pro Lys Pro Lys Pro Asn Ala Pro Thr  
                     980                      985                      990  
 Gln Arg Pro Pro Gly Arg Leu Gly Arg Trp Ile Arg Thr Val Ser Asp  
                     995                      1000                      1005  
 Glu Asp Leu Glu  
                     1010

<210> 78  
 <211> 1012  
 <212> PRT  
 <213> Infectious bursal disease virus  
  
 <220>  
 <221> DOMAIN  
 <222> (1)..(1012)  
 <223> Sequence of IBDV polyprotein CEF94-PP

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                     20                    25                    30  
 Leu Glu Lys His Thr Leu Arg Ser Glu Thr Ser Thr Tyr Asn Leu Thr  
                     35                    40                    45  
 Val Gly Asp Thr Gly Ser Gly Leu Ile Val Phe Phe Pro Gly Phe Pro  
                     50                    55                    60  
 Gly Ser Ile Val Gly Ala His Tyr Thr Leu Gln Ser Asn Gly Asn Tyr  
   65                    70                    75                    80  
 Lys Phe Asp Gln Met Leu Leu Thr Ala Gln Asn Leu Pro Ala Ser Tyr  
                     85                    90                    95  
 Asn Tyr Cys Arg Leu Val Ser Arg Ser Leu Thr Val Arg Ser Ser Thr  
                     100                    105                    110  
 Leu Pro Gly Gly Val Tyr Ala Leu Asn Gly Thr Ile Asn Ala Val Thr  
                     115                    120                    125  
 Phe Gln Gly Ser Leu Ser Glu Leu Thr Asp Val Ser Tyr Asn Gly Leu  
   130                    135                    140

Met Ser Ala Thr Ala Asn Ile Asn Asp Lys Ile Gly Asn Val Leu Val  
 145 150 155 160  
 Gly Glu Gly Val Thr Val Leu Ser Leu Pro Thr Ser Tyr Asp Leu Gly  
 165 170 175  
 Tyr Val Arg Leu Gly Asp Pro Ile Pro Ala Ile Gly Leu Asp Pro Lys  
 180 185 190  
 Met Val Ala Thr Cys Asp Ser Ser Asp Arg Pro Arg Val Tyr Thr Ile  
 195 200 205  
 Thr Ala Ala Asp Asp Tyr Gln Phe Ser Ser Gln Tyr Gln Pro Gly Gly  
 210 215 220  
 Val Thr Ile Thr Leu Phe Ser Ala Asn Ile Asp Ala Ile Thr Ser Leu  
 225 230 235 240  
 Ser Val Gly Gly Glu Leu Val Phe Gln Thr Ser Val His Gly Leu Val  
 245 250 255  
 Leu Gly Ala Thr Ile Tyr Leu Ile Gly Phe Asp Gly Thr Ala Val Ile  
 260 265 270  
 Thr Arg Ala Val Ala Ala Asn Asn Gly Leu Thr Thr Gly Thr Asp Asn  
 275 280 285  
 Leu Leu Pro Phe Asn Leu Val Ile Pro Thr Asn Glu Ile Thr Gln Pro  
 290 295 300  
 Ile Thr Ser Ile Lys Leu Glu Ile Val Thr Ser Lys Ser Gly Gly Gln  
 305 310 315 320  
 Ala Gly Asp Gln Met Ser Trp Ser Ala Arg Gly Ser Leu Ala Val Thr  
 325 330 335  
 Ile His Gly Gly Asn Tyr Pro Gly Ala Leu Arg Pro Val Thr Leu Val  
 340 345 350  
 Ala Tyr Glu Arg Val Ala Thr Gly Ser Val Val Thr Val Ala Gly Val  
 355 360 365  
 Ser Asn Phe Glu Leu Ile Pro Asn Pro Glu Leu Ala Lys Asn Leu Val  
 370 375 380  
 Thr Glu Tyr Gly Arg Phe Asp Pro Gly Ala Met Asn Tyr Thr Lys Leu  
 385 390 395 400  
 Ile Leu Ser Glu Arg Asp Arg Leu Gly Ile Lys Thr Val Trp Pro Thr  
 405 410 415  
 Arg Glu Tyr Thr Asp Phe Arg Glu Tyr Phe Met Glu Val Ala Asp Leu  
 420 425 430

Asn Ser Pro Leu Lys Ile Ala Gly Ala Phe Gly Phe Lys Asp Ile Ile  
 435 440 445  
 Arg Ala Ile Arg Arg Ile Ala Val Pro Val Val Ser Thr Leu Phe Pro  
 450 455 460  
 Pro Ala Ala Pro Leu Ala His Ala Ile Gly Glu Gly Val Asp Tyr Leu  
 465 470 475 480  
 Leu Gly Asp Glu Ala Gln Ala Ala Ser Gly Thr Ala Arg Ala Ala Ser  
 485 490 495  
 Gly Lys Ala Arg Ala Ala Ser Gly Arg Ile Arg Gln Leu Thr Leu Ala  
 500 505 510  
 Ala Asp Lys Gly Tyr Glu Val Val Ala Asn Leu Phe Gln Val Pro Gln  
 515 520 525  
 Asn Pro Val Val Asp Gly Ile Leu Ala Ser Pro Gly Val Leu Arg Gly  
 530 535 540  
 Ala His Asn Leu Asp Cys Val Leu Arg Glu Gly Ala Thr Leu Phe Pro  
 545 550 555 560  
 Val Val Ile Thr Thr Val Glu Asp Ala Met Thr Pro Lys Ala Leu Asn  
 565 570 575  
 Ser Lys Met Phe Ala Val Ile Glu Gly Val Arg Glu Asp Leu Gln Pro  
 580 585 590  
 Pro Ser Gln Arg Gly Ser Phe Ile Arg Thr Leu Ser Gly His Arg Val  
 595 600 605  
 Tyr Gly Tyr Ala Pro Asp Gly Val Leu Pro Leu Glu Thr Gly Arg Asp  
 610 615 620  
 Tyr Thr Val Val Pro Ile Asp Asp Val Trp Asp Asp Ser Ile Met Leu  
 625 630 635 640  
 Ser Lys Asp Pro Ile Pro Pro Ile Val Gly Asn Ser Gly Asn Leu Ala  
 645 650 655  
 Ile Ala Tyr Met Asp Val Phe Arg Pro Lys Val Pro Ile His Val Ala  
 660 665 670  
 Met Thr Gly Ala Leu Asn Ala Cys Gly Glu Ile Glu Lys Val Ser Phe  
 675 680 685  
 Arg Ser Thr Lys Leu Ala Thr Ala His Arg Leu Gly Leu Lys Leu Ala  
 690 695 700  
 Gly Pro Gly Ala Phe Asp Val Asn Thr Gly Pro Asn Trp Ala Thr Phe  
 705 710 715 720  
 Ile Lys Arg Phe Pro His Asn Pro Arg Asp Trp Asp Arg Leu Pro Tyr



<210> 79  
 <211> 1012  
 <212> PRT  
 <213> Infectious bursal disease virus  
  
 <220>  
 <221> DOMAIN  
 <222> (1)..(1012)  
 <223> Sequence of IBDV polyprotein D6948-PP  
  
 <400> 79  
 Met Thr Asn Leu Gln Asp Gln Thr Gln Gln Ile Val Pro Phe Ile Arg  
   1                  5                  10                  15  
  
 Ser Leu Leu Met Pro Thr Thr Gly Pro Ala Ser Ile Pro Asp Asp Thr  
           20                  25                  30  
  
 Leu Glu Lys His Thr Leu Arg Ser Glu Thr Ser Thr Tyr Asn Leu Thr  
           35                  40                  45  
  
 Val Gly Asp Thr Gly Ser Gly Leu Ile Val Phe Phe Pro Gly Phe Pro  
   50                  55                  60  
  
 Gly Ser Ile Val Gly Ala His Tyr Thr Leu Gln Ser Asn Gly Asn Tyr  
   65                  70                  75                  80  
  
 Lys Phe Asp Gln Met Leu Leu Thr Ala Gln Asn Leu Pro Ala Ser Tyr  
           85                  90                  95  
  
 Asn Tyr Cys Arg Leu Val Ser Arg Ser Leu Thr Val Arg Ser Ser Thr  
          100                 105                 110  
  
 Leu Pro Gly Gly Val Tyr Ala Leu Asn Gly Thr Ile Asn Ala Val Thr  
   115                 120                 125  
  
 Phe Gln Gly Ser Leu Ser Glu Leu Thr Asp Val Ser Tyr Asn Gly Leu  
   130                 135                 140  
  
 Met Ser Ala Thr Ala Asn Ile Asn Asp Lys Ile Gly Asn Val Leu Val  
 145                 150                 155                 160  
  
 Gly Glu Gly Val Thr Val Leu Ser Leu Pro Thr Ser Tyr Asp Leu Gly  
          165                 170                 175  
  
 Tyr Val Arg Leu Gly Asp Pro Ile Pro Ala Ile Gly Leu Asp Pro Lys  
          180                 185                 190  
  
 Met Val Ala Thr Cys Asp Ser Ser Asp Arg Pro Arg Val Tyr Thr Ile  
   195                 200                 205  
  
 Thr Ala Ala Asp Asp Tyr Gln Phe Ser Ser Gln Tyr Gln Ala Gly Gly  
   210                 215                 220



Val Thr Ile Thr Leu Phe Ser Ala Asn Ile Asp Ala Ile Thr Ser Leu  
225 230 235 240  
Ser Ile Gly Gly Glu Leu Val Phe Gln Thr Ser Val Gln Gly Leu Ile  
245 250 255  
Leu Gly Ala Thr Ile Tyr Leu Ile Gly Phe Asp Gly Thr Ala Val Ile  
260 265 270  
Thr Arg Ala Val Ala Ala Asp Asn Gly Leu Thr Ala Gly Thr Asp Asn  
275 280 285  
Leu Met Pro Phe Asn Ile Val Ile Pro Thr Ser Glu Ile Thr Gln Pro  
290 295 300  
Ile Thr Ser Ile Lys Leu Glu Ile Val Thr Ser Lys Ser Gly Gly Gln  
305 310 315 320  
Ala Gly Asp Gln Met Ser Trp Ser Ala Ser Gly Ser Leu Ala Val Thr  
325 330 335  
Ile His Gly Gly Asn Tyr Pro Gly Ala Leu Arg Pro Val Thr Leu Val  
340 345 350  
Ala Tyr Glu Arg Val Ala Thr Gly Ser Val Val Thr Val Ala Gly Val  
355 360 365  
Ser Asn Phe Glu Leu Ile Pro Asn Pro Glu Leu Ala Lys Asn Leu Val  
370 375 380  
Thr Glu Tyr Gly Arg Phe Asp Pro Gly Ala Met Asn Tyr Thr Lys Leu  
385 390 395 400  
Ile Leu Ser Glu Arg Asp Arg Leu Gly Ile Lys Thr Val Trp Pro Thr  
405 410 415  
Arg Glu Tyr Thr Asp Phe Arg Glu Tyr Phe Met Glu Val Ala Asp Leu  
420 425 430  
Asn Ser Pro Leu Lys Ile Ala Gly Ala Phe Gly Phe Lys Asp Ile Ile  
435 440 445  
Arg Ala Leu Arg Arg Ile Ala Val Pro Val Val Ser Thr Leu Phe Pro  
450 455 460  
Pro Ala Ala Pro Leu Ala His Ala Ile Gly Glu Gly Val Asp Tyr Leu  
465 470 475 480  
Leu Gly Asp Glu Ala Gln Ala Ala Ser Gly Thr Ala Arg Ala Ala Ser  
485 490 495  
Gly Lys Ala Arg Ala Ala Ser Gly Arg Ile Arg Gln Leu Thr Leu Ala  
500 505 510  
Ala Asp Lys Gly Tyr Glu Val Val Ala Asn Leu Phe Gln Val Pro Gln

515					520					525					
Asn	Pro	Val	Val	Asp	Gly	Ile	Leu	Ala	Ser	Pro	Gly	Ile	Leu	Arg	Gly
530						535					540				
Ala	His	Asn	Leu	Asp	Cys	Val	Leu	Arg	Glu	Gly	Ala	Thr	Leu	Phe	Pro
545					550					555					560
Val	Val	Ile	Thr	Thr	Val	Glu	Asp	Ala	Met	Thr	Pro	Lys	Ala	Leu	Asn
				565					570					575	
Ser	Lys	Met	Phe	Ala	Val	Ile	Glu	Gly	Val	Arg	Glu	Asp	Leu	Gln	Pro
			580					585					590		
Pro	Ser	Gln	Arg	Gly	Ser	Phe	Ile	Arg	Thr	Leu	Ser	Gly	His	Arg	Val
		595					600					605			
Tyr	Gly	Tyr	Ala	Pro	Asp	Gly	Val	Leu	Pro	Leu	Glu	Thr	Gly	Arg	Asp
610						615					620				
Tyr	Thr	Val	Val	Pro	Ile	Asp	Asp	Val	Trp	Asp	Asp	Ser	Ile	Met	Leu
625					630					635					640
Ser	Lys	Asp	Pro	Ile	Pro	Pro	Ile	Val	Gly	Asn	Ser	Gly	Asn	Leu	Ala
				645					650					655	
Ile	Ala	Tyr	Met	Asp	Val	Phe	Arg	Pro	Lys	Val	Pro	Ile	His	Val	Ala
			660					665					670		
Met	Thr	Gly	Ala	Leu	Asn	Ala	Tyr	Gly	Glu	Ile	Glu	Asn	Val	Ser	Phe
		675					680					685			
Arg	Ser	Thr	Lys	Leu	Ala	Thr	Ala	His	Arg	Leu	Gly	Leu	Lys	Leu	Ala
						695					700				
Gly	Pro	Gly	Ala	Phe	Asp	Val	Asn	Thr	Gly	Ser	Asn	Trp	Ala	Thr	Phe
705					710					715					720
Ile	Lys	Arg	Phe	Pro	His	Asn	Pro	Arg	Asp	Trp	Asp	Arg	Leu	Pro	Tyr
				725					730					735	
Leu	Asn	Leu	Pro	Tyr	Leu	Pro	Pro	Asn	Ala	Gly	Arg	Gln	Tyr	Asp	Leu
			740					745					750		
Ala	Met	Ala	Ala	Ser	Glu	Phe	Lys	Glu	Thr	Pro	Glu	Leu	Glu	Ser	Ala
		755					760					765			
Val	Arg	Ala	Met	Glu	Ala	Ala	Ala	Asn	Val	Asp	Pro	Leu	Phe	Gln	Ser
	770					775					780				
Ala	Leu	Ser	Val	Phe	Met	Trp	Leu	Glu	Glu	Asn	Gly	Ile	Val	Thr	Asp
785					790					795					800
Met	Ala	Asn	Phe	Ala	Leu	Ser	Asp	Pro	Asn	Ala	His	Arg	Met	Arg	Asn
				805					810					815	

Phe Leu Ala Asn Ala Pro Gln Ala Gly Ser Lys Ser Gln Arg Ala Lys  
                   820                                  825                                  830  
 Tyr Gly Thr Ala Gly Tyr Gly Val Glu Ala Arg Gly Pro Thr Pro Glu  
                   835                                  840                                  845  
 Glu Ala Gln Arg Glu Lys Asp Thr Arg Ile Ser Lys Lys Met Glu Thr  
                   850                                  855                                  860  
 Met Gly Ile Tyr Phe Ala Thr Pro Glu Trp Val Ala Leu Asn Gly His  
 865                                  870                                  875                                  880  
 Arg Gly Pro Ser Pro Gly Gln Leu Lys Tyr Trp Gln Asn Thr Arg Glu  
                                   885                                  890                                  895  
 Ile Pro Asp Pro Asn Glu Asp Tyr Leu Asp Tyr Val His Ala Glu Lys  
                   900                                  905                                  910  
 Ser Arg Leu Ala Ser Glu Glu Gln Ile Leu Arg Ala Ala Thr Ser Ile  
                   915                                  920                                  925  
 Tyr Gly Ala Pro Gly Gln Ala Glu Pro Pro Gln Ala Phe Ile Asp Glu  
                   930                                  935                                  940  
 Val Ala Lys Val Tyr Glu Ile Asn His Gly Arg Gly Pro Asn Gln Glu  
 945                                  950                                  955                                  960  
 Gln Met Lys Asp Leu Leu Leu Thr Ala Met Glu Met Lys His Arg Asn  
                                   965                                  970                                  975  
 Pro Arg Arg Ala Pro Pro Lys Pro Lys Pro Lys Pro Asn Ala Pro Thr  
                   980                                  985                                  990  
 Gln Arg Pro Pro Gly Arg Leu Gly Arg Trp Ile Arg Ala Val Ser Asp  
                   995                                  1000                                  1005  
 Glu Asp Leu Glu  
                   1010

<210> 80  
 <211> 290  
 <212> PRT  
 <213> Infectious bursal disease virus

<220>  
 <221> DOMAIN  
 <222> (1)..(290)  
 <223> Sequence of IBDV polyprotein TY89-PP

<400> 80  
 Arg Phe Pro His Asn Pro Arg Asp Trp Asp Arg Leu Pro Tyr Leu Asn  
   1                                  5                                  10                                  15

Leu Pro Tyr Leu Pro Pro Thr Ala Gly Arg Gln Phe His Leu Ala Leu  
 20 25 30  
 Ala Ala Ser Glu Phe Lys Glu Thr Pro Glu Leu Glu Asp Ala Val Arg  
 35 40 45  
 Ala Met Asp Ala Ala Ala Asn Val Asp Pro Leu Phe Arg Ser Ala Leu  
 50 55 60  
 Gln Val Phe Met Trp Leu Glu Glu Asn Gly Ile Val Thr Asp Met Ala  
 65 70 75 80  
 Asn Phe Ala Leu Ser Asp Pro Asn Ala His Arg Met Lys Asn Phe Leu  
 85 90 95  
 Ala Asn Ala Pro Gln Ala Gly Ser Lys Ser Gln Arg Ala Lys Tyr Gly  
 100 105 110  
 Thr Ala Gly Tyr Gly Val Glu Ala Arg Gly Pro Thr Pro Glu Glu Ala  
 115 120 125  
 Gln Arg Glu Lys Asp Thr Arg Ile Ser Lys Lys Met Glu Thr Met Gly  
 130 135 140  
 Ile Tyr Phe Ala Thr Pro Glu Trp Val Ala Leu Asn Gly His Arg Gly  
 145 150 155 160  
 Pro Ser Pro Gly Gln Leu Lys Tyr Trp Gln Asn Thr Arg Glu Ile Pro  
 165 170 175  
 Glu Pro Asn Glu Asp Tyr Pro Asp Tyr Val His Ala Glu Lys Ser Arg  
 180 185 190  
 Leu Ala Ser Glu Glu Gln Val Leu Arg Ala Ala Thr Ser Ile Tyr Gly  
 195 200 205  
 Ala Pro Gly Gln Ala Glu Pro Pro Gln Ala Phe Ile Asp Glu Val Ala  
 210 215 220  
 Arg Val Tyr Glu Ile Asn His Gly Arg Gly Pro Asn Gln Glu Gln Met  
 225 230 235 240  
 Lys Asp Leu Leu Leu Thr Ala Met Glu Met Lys His Arg Asn Pro Arg  
 245 250 255  
 Arg Ala Pro Pro Lys Pro Lys Pro Lys Pro Asn Ala Pro Ser Gln Arg  
 260 265 270  
 Pro Pro Gly Arg Leu Gly Arg Trp Ile Arg Thr Val Ser Asp Glu Asp  
 275 280 285  
 Leu Glu  
 290

<210> 81  
 <211> 881  
 <212> PRT  
 <213> Infectious bursal disease virus

<220>  
 <221> DOMAIN  
 <222> (1)..(881)  
 <223> Consensus sequence of IBDV VP1, ~~whereby the Xaa~~  
~~indicator may be any amino acid~~

<220>  
 <221> MISC FEATURE  
 <222> (4)  
 <223> The 'Xaa' at position 4 may be any amino acid

<220>  
 <221> MISC FEATURE  
 <222> (13)  
 <223> The 'Xaa' at position 13 may be any amino acid

<220>  
 <221> MISC FEATURE  
 <222> (61)  
 <223> The 'Xaa' at position 61 may be any amino acid

<220>  
 <221> MISC FEATURE  
 <222> (145). . . (147)  
 <223> The 'Xaa' at positions 145-147 may be any amino acid

<220>  
 <221> MISC FEATURE  
 <222> (242)  
 <223> The 'Xaa' at position 242 may be any amino acid

<220>  
 <221> MISC FEATURE  
 <222> (287)  
 <223> The 'Xaa' at position 287 may be any amino acid

<220>  
 <221> MISC FEATURE  
 <222> (390)  
 <223> The 'Xaa' at position 390 may be any amino acid

<220>  
 <221> MISC FEATURE  
 <222> (393)  
 <223> The 'Xaa' at position 393 may be any amino acid

<220>  
 <221> MISC FEATURE  
 <222> (508)

<223> The 'Xaa' at position 508 may be any amino acid

<220>

<221> MISC FEATURE

<222> (511)

<223> The 'Xaa' at position 511 may be any amino acid

<220>

<221> MISC FEATURE

<222> (546)

<223> The 'Xaa' at position 546 may be any amino acid

<220>

<221> MISC FEATURE

<222> (562)

<223> The 'Xaa' at position 562 may be any amino acid

<220>

<221> MISC FEATURE

<222> (646)

<223> The 'Xaa' at position 646 may be any amino acid

<220>

<221> MISC FEATURE

<222> (687)

<223> The 'Xaa' at position 687 may be any amino acid

<220>

<221> MISC FEATURE

<222> (695)

<223> The 'Xaa' at position 695 may be any amino acid

<220>

<221> MISC FEATURE

<222> (880) . . . (881)

<223> The 'Xaa' at positions 880-881 may be any amino acid

<400> 81

Met Ser Asp Xaa Phe Asn Ser Pro Gln Ala Arg Ser Xaa Ile Ser Ala  
1 5 10 15

Ala Phe Gly Ile Lys Pro Thr Ala Gly Gln Asp Val Glu Glu Leu Leu  
20 25 30

Ile Pro Lys Val Trp Val Pro Pro Glu Asp Pro Leu Ala Ser Pro Ser  
35 40 45

Arg Leu Ala Lys Phe Leu Arg Glu Asn Gly Tyr Lys Xaa Leu Gln Pro  
50 55 60

Arg Ser Leu Pro Glu Asn Glu Glu Tyr Glu Thr Asp Gln Ile Leu Pro  
65 70 75 80

Asp Leu Ala Trp Met Arg Gln Ile Glu Gly Ala Val Leu Lys Pro Thr  
85 90 95

Leu Ser Leu Pro Ile Gly Asp Gln Glu Tyr Phe Pro Lys Tyr Tyr Pro  
 100 105 110  
 Thr His Arg Pro Ser Lys Glu Lys Pro Asn Ala Tyr Pro Pro Asp Ile  
 115 120 125  
 Ala Leu Leu Lys Gln Met Ile Tyr Leu Phe Leu Gln Val Pro Glu Ala  
 130 135 140  
 Xaa Xaa Xaa Leu Lys Asp Glu Val Thr Leu Leu Thr Gln Asn Ile Arg  
 145 150 155 160  
 Asp Lys Ala Tyr Gly Ser Gly Thr Tyr Met Gly Gln Ala Thr Arg Leu  
 165 170 175  
 Val Ala Met Lys Glu Val Ala Thr Gly Arg Asn Pro Asn Lys Asp Pro  
 180 185 190  
 Leu Lys Leu Gly Tyr Thr Phe Glu Ser Ile Ala Gln Leu Leu Asp Ile  
 195 200 205  
 Thr Leu Pro Val Gly Pro Pro Gly Glu Asp Asp Lys Pro Trp Val Pro  
 210 215 220  
 Leu Thr Arg Val Pro Ser Arg Met Leu Val Leu Thr Gly Asp Val Asp  
 225 230 235 240  
 Gly Xaa Phe Glu Val Glu Asp Tyr Leu Pro Lys Ile Asn Leu Lys Ser  
 245 250 255  
 Ser Ser Gly Leu Pro Tyr Val Gly Arg Thr Lys Gly Glu Thr Ile Gly  
 260 265 270  
 Glu Met Ile Ala Ile Ser Asn Gln Phe Leu Arg Glu Leu Ser Xaa Leu  
 275 280 285  
 Leu Lys Gln Gly Ala Gly Thr Lys Gly Ser Asn Lys Lys Lys Leu Leu  
 290 295 300  
 Ser Met Leu Ser Asp Tyr Trp Tyr Leu Ser Cys Gly Leu Leu Phe Pro  
 305 310 315 320  
 Lys Ala Glu Arg Tyr Asp Lys Ser Thr Trp Leu Thr Lys Thr Arg Asn  
 325 330 335  
 Ile Trp Ser Ala Pro Ser Pro Thr His Leu Met Ile Ser Met Ile Thr  
 340 345 350  
 Trp Pro Val Met Ser Asn Ser Pro Asn Asn Val Leu Asn Ile Glu Gly  
 355 360 365  
 Cys Pro Ser Leu Tyr Lys Phe Asn Pro Phe Arg Gly Gly Leu Asn Arg  
 370 375 380

Ile Val Glu Trp Ile Xaa Ala Pro Xaa Glu Pro Lys Ala Leu Val Tyr  
 385 390 395 400  
 Ala Asp Asn Ile Tyr Ile Val His Ser Asn Thr Trp Tyr Ser Ile Asp  
 405 410 415  
 Leu Glu Lys Gly Glu Ala Asn Cys Thr Arg Gln His Met Gln Ala Ala  
 420 425 430  
 Met Tyr Tyr Ile Leu Thr Arg Gly Trp Ser Asp Asn Gly Asp Pro Met  
 435 440 445  
 Phe Asn Gln Thr Trp Ala Thr Phe Ala Met Asn Ile Ala Pro Ala Leu  
 450 455 460  
 Val Val Asp Ser Ser Cys Leu Ile Met Asn Leu Gln Ile Lys Thr Tyr  
 465 470 475 480  
 Gly Gln Gly Ser Gly Asn Ala Ala Thr Phe Ile Asn Asn His Leu Leu  
 485 490 495  
 Ser Thr Leu Val Leu Asp Gln Trp Asn Leu Met Xaa Gln Pro Xaa Pro  
 500 505 510  
 Asp Ser Glu Glu Phe Lys Ser Ile Glu Asp Lys Leu Gly Ile Asn Phe  
 515 520 525  
 Lys Ile Glu Arg Ser Ile Asp Asp Ile Arg Gly Lys Leu Arg Gln Leu  
 530 535 540  
 Val Xaa Leu Ala Gln Pro Gly Tyr Leu Ser Gly Gly Val Glu Pro Glu  
 545 550 555 560  
 Gln Xaa Ser Pro Thr Val Glu Leu Asp Leu Leu Gly Trp Ser Ala Thr  
 565 570 575  
 Tyr Ser Lys Asp Leu Gly Ile Tyr Val Pro Val Leu Asp Lys Glu Arg  
 580 585 590  
 Leu Phe Cys Ser Ala Ala Tyr Pro Lys Gly Val Glu Asn Lys Ser Leu  
 595 600 605  
 Lys Ser Lys Val Gly Ile Glu Gln Ala Tyr Lys Val Val Arg Tyr Glu  
 610 615 620  
 Ala Leu Arg Leu Val Gly Gly Trp Asn Tyr Pro Leu Leu Asn Lys Ala  
 625 630 635 640  
 Cys Lys Asn Asn Ala Xaa Ala Ala Arg Arg His Leu Glu Ala Lys Gly  
 645 650 655  
 Phe Pro Leu Asp Glu Phe Leu Ala Glu Trp Ser Glu Leu Ser Glu Phe  
 660 665 670  
 Gly Glu Ala Phe Glu Gly Phe Asn Ile Lys Leu Thr Val Thr Xaa Glu



675	680	685
Ser Leu Ala Glu Leu Asn Xaa Pro Val Pro Pro Lys Pro Pro Asn Val		
690	695	700
Asn Arg Pro Val Asn Thr Gly Gly Leu Lys Ala Val Ser Asn Ala Leu		
705	710	715
Lys Thr Gly Arg Tyr Arg Asn Glu Ala Gly Leu Ser Gly Leu Val Leu		
	725	730
		735
Leu Ala Thr Ala Arg Ser Arg Leu Gln Asp Ala Val Lys Ala Lys Ala		
	740	745
		750
Glu Ala Glu Lys Leu His Lys Ser Lys Pro Asp Asp Pro Asp Ala Asp		
	755	760
		765
Trp Phe Glu Arg Ser Glu Thr Leu Ser Asp Leu Leu Glu Lys Ala Asp		
	770	775
		780
Ile Ala Ser Lys Val Ala His Ser Ala Leu Val Glu Thr Ser Asp Ala		
785	790	795
		800
Leu Glu Ala Val Gln Ser Thr Ser Val Tyr Thr Pro Lys Tyr Pro Glu		
	805	810
		815
Val Lys Asn Pro Gln Thr Ala Ser Asn Pro Val Val Gly Leu His Leu		
	820	825
		830
Pro Ala Lys Arg Ala Thr Gly Val Gln Ala Ala Leu Leu Gly Ala Gly		
	835	840
		845
Thr Ser Arg Pro Met Gly Met Glu Ala Pro Thr Arg Ser Lys Asn Ala		
	850	855
		860
Val Lys Met Ala Lys Arg Arg Gln Arg Gln Lys Glu Ser Arg Gln Xaa		
865	870	875
		880

Xaa

<210> 82  
 <211> 881  
 <212> PRT  
 <213> Infectious bursal disease virus

<220>  
 <221> DOMAIN  
 <222> (1)..(881)  
 <223> Sequence of IBDV CEF94-VP1

<400> 82  
 Met Ser Asp Ile Phe Asn Ser Pro Gln Ala Arg Ser Thr Ile Ser Ala  
 1 5 10 15

Ala Phe Gly Ile Lys Pro Thr Ala Gly Gln Asp Val Glu Glu Leu Leu  
 20 25 30  
 Ile Pro Lys Val Trp Val Pro Pro Glu Asp Pro Leu Ala Ser Pro Ser  
 35 40 45  
 Arg Leu Ala Lys Phe Leu Arg Glu Asn Gly Tyr Lys Val Leu Gln Pro  
 50 55 60  
 Arg Ser Leu Pro Glu Asn Glu Glu Tyr Glu Thr Asp Gln Ile Leu Pro  
 65 70 75 80  
 Asp Leu Ala Trp Met Arg Gln Ile Glu Gly Ala Val Leu Lys Pro Thr  
 85 90 95  
 Leu Ser Leu Pro Ile Gly Asp Gln Glu Tyr Phe Pro Lys Tyr Tyr Pro  
 100 105 110  
 Thr His Arg Pro Ser Lys Glu Lys Pro Asn Ala Tyr Pro Pro Asp Ile  
 115 120 125  
 Ala Leu Leu Lys Gln Met Ile Tyr Leu Phe Leu Gln Val Pro Glu Ala  
 130 135 140  
 Asn Glu Gly Leu Lys Asp Glu Val Thr Leu Leu Thr Gln Asn Ile Arg  
 145 150 155 160  
 Asp Lys Ala Tyr Gly Ser Gly Thr Tyr Met Gly Gln Ala Thr Arg Leu  
 165 170 175  
 Val Ala Met Lys Glu Val Ala Thr Gly Arg Asn Pro Asn Lys Asp Pro  
 180 185 190  
 Leu Lys Leu Gly Tyr Thr Phe Glu Ser Ile Ala Gln Leu Leu Asp Ile  
 195 200 205  
 Thr Leu Pro Val Gly Pro Pro Gly Glu Asp Asp Lys Pro Trp Val Pro  
 210 215 220  
 Leu Thr Arg Val Pro Ser Arg Met Leu Val Leu Thr Gly Asp Val Asp  
 225 230 235 240  
 Gly Asp Phe Glu Val Glu Asp Tyr Leu Pro Lys Ile Asn Leu Lys Ser  
 245 250 255  
 Ser Ser Gly Leu Pro Tyr Val Gly Arg Thr Lys Gly Glu Thr Ile Gly  
 260 265 270  
 Glu Met Ile Ala Ile Ser Asn Gln Phe Leu Arg Glu Leu Ser Thr Leu  
 275 280 285  
 Leu Lys Gln Gly Ala Gly Thr Lys Gly Ser Asn Lys Lys Lys Leu Leu  
 290 295 300  
 Ser Met Leu Ser Asp Tyr Trp Tyr Leu Ser Cys Gly Leu Leu Phe Pro

305					310						315				320
Lys	Ala	Glu	Arg	Tyr	Asp	Lys	Ser	Thr	Trp	Leu	Thr	Lys	Thr	Arg	Asn
				325					330					335	
Ile	Trp	Ser	Ala	Pro	Ser	Pro	Thr	His	Leu	Met	Ile	Ser	Met	Ile	Thr
			340					345					350		
Trp	Pro	Val	Met	Ser	Asn	Ser	Pro	Asn	Asn	Val	Leu	Asn	Ile	Glu	Gly
		355					360					365			
Cys	Pro	Ser	Leu	Tyr	Lys	Phe	Asn	Pro	Phe	Arg	Gly	Gly	Leu	Asn	Arg
	370					375					380				
Ile	Val	Glu	Trp	Ile	Leu	Ala	Pro	Glu	Glu	Pro	Lys	Ala	Leu	Val	Tyr
385					390					395					400
Ala	Asp	Asn	Ile	Tyr	Ile	Val	His	Ser	Asn	Thr	Trp	Tyr	Ser	Ile	Asp
				405					410					415	
Leu	Glu	Lys	Gly	Glu	Ala	Asn	Cys	Thr	Arg	Gln	His	Met	Gln	Ala	Ala
			420					425					430		
Met	Tyr	Tyr	Ile	Leu	Thr	Arg	Gly	Trp	Ser	Asp	Asn	Gly	Asp	Pro	Met
		435					440					445			
Phe	Asn	Gln	Thr	Trp	Ala	Thr	Phe	Ala	Met	Asn	Ile	Ala	Pro	Ala	Leu
	450					455					460				
Val	Val	Asp	Ser	Ser	Cys	Leu	Ile	Met	Asn	Leu	Gln	Ile	Lys	Thr	Tyr
465					470					475					480
Gly	Gln	Gly	Ser	Gly	Asn	Ala	Ala	Thr	Phe	Ile	Asn	Asn	His	Leu	Leu
				485					490					495	
Ser	Thr	Leu	Val	Leu	Asp	Gln	Trp	Asn	Leu	Met	Arg	Gln	Pro	Arg	Pro
			500					505					510		
Asp	Ser	Glu	Glu	Phe	Lys	Ser	Ile	Glu	Asp	Lys	Leu	Gly	Ile	Asn	Phe
		515					520					525			
Lys	Ile	Glu	Arg	Ser	Ile	Asp	Asp	Ile	Arg	Gly	Lys	Leu	Arg	Gln	Leu
	530					535					540				
Val	Leu	Leu	Ala	Gln	Pro	Gly	Tyr	Leu	Ser	Gly	Gly	Val	Glu	Pro	Glu
545					550					555					560
Gln	Ser	Ser	Pro	Thr	Val	Glu	Leu	Asp	Leu	Leu	Gly	Trp	Ser	Ala	Thr
				565					570					575	
Tyr	Ser	Lys	Asp	Leu	Gly	Ile	Tyr	Val	Pro	Val	Leu	Asp	Lys	Glu	Arg
			580					585					590		
Leu	Phe	Cys	Ser	Ala	Ala	Tyr	Pro	Lys	Gly	Val	Glu	Asn	Lys	Ser	Leu
		595					600					605			

Lys Ser Lys Val Gly Ile Glu Gln Ala Tyr Lys Val Val Arg Tyr Glu  
 610 615 620  
 Ala Leu Arg Leu Val Gly Gly Trp Asn Tyr Pro Leu Leu Asn Lys Ala  
 625 630 635 640  
 Cys Lys Asn Asn Ala Gly Ala Ala Arg Arg His Leu Glu Ala Lys Gly  
 645 650 655  
 Phe Pro Leu Asp Glu Phe Leu Ala Glu Trp Ser Glu Leu Ser Glu Phe  
 660 665 670  
 Gly Glu Ala Phe Glu Gly Phe Asn Ile Lys Leu Thr Val Thr Ser Glu  
 675 680 685  
 Ser Leu Ala Glu Leu Asn Lys Pro Val Pro Pro Lys Pro Pro Asn Val  
 690 695 700  
 Asn Arg Pro Val Asn Thr Gly Gly Leu Lys Ala Val Ser Asn Ala Leu  
 705 710 715 720  
 Lys Thr Gly Arg Tyr Arg Asn Glu Ala Gly Leu Ser Gly Leu Val Leu  
 725 730 735  
 Leu Ala Thr Ala Arg Ser Arg Leu Gln Asp Ala Val Lys Ala Lys Ala  
 740 745 750  
 Glu Ala Glu Lys Leu His Lys Ser Lys Pro Asp Asp Pro Asp Ala Asp  
 755 760 765  
 Trp Phe Glu Arg Ser Glu Thr Leu Ser Asp Leu Leu Glu Lys Ala Asp  
 770 775 780  
 Ile Ala Ser Lys Val Ala His Ser Ala Leu Val Glu Thr Ser Asp Ala  
 785 790 795 800  
 Leu Glu Ala Val Gln Ser Thr Ser Val Tyr Thr Pro Lys Tyr Pro Glu  
 805 810 815  
 Val Lys Asn Pro Gln Thr Ala Ser Asn Pro Val Val Gly Leu His Leu  
 820 825 830  
 Pro Ala Lys Arg Ala Thr Gly Val Gln Ala Ala Leu Leu Gly Ala Gly  
 835 840 845  
 Thr Ser Arg Pro Met Gly Met Glu Ala Pro Thr Arg Ser Lys Asn Ala  
 850 855 860  
 Val Lys Met Ala Lys Arg Arg Gln Arg Gln Lys Glu Ser Arg Gln Gln  
 865 870 875 880  
 Pro

<210> 83  
 <211> 879  
 <212> PRT  
 <213> Infectious bursal disease virus  
  
 <220>  
 <221> DOMAIN  
 <222> (1)..(879)  
 <223> Sequence of IBDV D6948-VP1  
  
 <400> 83  
 Met Ser Asp Val Phe Asn Ser Pro Gln Ala Arg Ser Lys Ile Ser Ala  
   1                  5                  10                  15  
  
 Ala Phe Gly Ile Lys Pro Thr Ala Gly Gln Asp Val Glu Glu Leu Leu  
           20                  25                  30  
  
 Ile Pro Lys Val Trp Val Pro Pro Glu Asp Pro Leu Ala Ser Pro Ser  
           35                  40                  45  
  
 Arg Leu Ala Lys Phe Leu Arg Glu Asn Gly Tyr Lys Ile Leu Gln Pro  
   50                  55                  60  
  
 Arg Ser Leu Pro Glu Asn Glu Glu Tyr Glu Thr Asp Gln Ile Leu Pro  
   65                  70                  75                  80  
  
 Asp Leu Ala Trp Met Arg Gln Ile Glu Gly Ala Val Leu Lys Pro Thr  
           85                  90                  95  
  
 Leu Ser Leu Pro Ile Gly Asp Gln Glu Tyr Phe Pro Lys Tyr Tyr Pro  
          100                 105                 110  
  
 Thr His Arg Pro Ser Lys Glu Lys Pro Asn Ala Tyr Pro Pro Asp Ile  
          115                 120                 125  
  
 Ala Leu Leu Lys Gln Met Ile Tyr Leu Phe Leu Gln Val Pro Glu Ala  
   130                 135                 140  
  
 Thr Asp Asn Leu Lys Asp Glu Val Thr Leu Leu Thr Gln Asn Ile Arg  
  145                 150                 155                 160  
  
 Asp Lys Ala Tyr Gly Ser Gly Thr Tyr Met Gly Gln Ala Thr Arg Leu  
          165                 170                 175  
  
 Val Ala Met Lys Glu Val Ala Thr Gly Arg Asn Pro Asn Lys Asp Pro  
          180                 185                 190  
  
 Leu Lys Leu Gly Tyr Thr Phe Glu Ser Ile Ala Gln Leu Leu Asp Ile  
   195                 200                 205  
  
 Thr Leu Pro Val Gly Pro Pro Gly Glu Asp Asp Lys Pro Trp Val Pro  
   210                 215                 220  
  
 Leu Thr Arg Val Pro Ser Arg Met Leu Val Leu Thr Gly Asp Val Asp  
  225                 230                 235                 240

Gly Glu Phe Glu Val Glu Asp Tyr Leu Pro Lys Ile Asn Leu Lys Ser  
 245 250 255  
 Ser Ser Gly Leu Pro Tyr Val Gly Arg Thr Lys Gly Glu Thr Ile Gly  
 260 265 270  
 Glu Met Ile Ala Ile Ser Asn Gln Phe Leu Arg Glu Leu Ser Ala Leu  
 275 280 285  
 Leu Lys Gln Gly Ala Gly Thr Lys Gly Ser Asn Lys Lys Lys Leu Leu  
 290 295 300  
 Ser Met Leu Ser Asp Tyr Trp Tyr Leu Ser Cys Gly Leu Leu Phe Pro  
 305 310 315 320  
 Lys Ala Glu Arg Tyr Asp Lys Ser Thr Trp Leu Thr Lys Thr Arg Asn  
 325 330 335  
 Ile Trp Ser Ala Pro Ser Pro Thr His Leu Met Ile Ser Met Ile Thr  
 340 345 350  
 Trp Pro Val Met Ser Asn Ser Pro Asn Asn Val Leu Asn Ile Glu Gly  
 355 360 365  
 Cys Pro Ser Leu Tyr Lys Phe Asn Pro Phe Arg Gly Gly Leu Asn Arg  
 370 375 380  
 Ile Val Glu Trp Ile Met Ala Pro Asp Glu Pro Lys Ala Leu Val Tyr  
 385 390 395 400  
 Ala Asp Asn Ile Tyr Ile Val His Ser Asn Thr Trp Tyr Ser Ile Asp  
 405 410 415  
 Leu Glu Lys Gly Glu Ala Asn Cys Thr Arg Gln His Met Gln Ala Ala  
 420 425 430  
 Met Tyr Tyr Ile Leu Thr Arg Gly Trp Ser Asp Asn Gly Asp Pro Met  
 435 440 445  
 Phe Asn Gln Thr Trp Ala Thr Phe Ala Met Asn Ile Ala Pro Ala Leu  
 450 455 460  
 Val Val Asp Ser Ser Cys Leu Ile Met Asn Leu Gln Ile Lys Thr Tyr  
 465 470 475 480  
 Gly Gln Gly Ser Gly Asn Ala Ala Thr Phe Ile Asn Asn His Leu Leu  
 485 490 495  
 Ser Thr Leu Val Leu Asp Gln Trp Asn Leu Met Lys Gln Pro Ser Pro  
 500 505 510  
 Asp Ser Glu Glu Phe Lys Ser Ile Glu Asp Lys Leu Gly Ile Asn Phe  
 515 520 525

Lys Ile Glu Arg Ser Ile Asp Asp Ile Arg Gly Lys Leu Arg Gln Leu  
 530 535 540  
 Val Pro Leu Ala Gln Pro Gly Tyr Leu Ser Gly Gly Val Glu Pro Glu  
 545 550 555 560  
 Gln Pro Ser Pro Thr Val Glu Leu Asp Leu Leu Gly Trp Ser Ala Thr  
 565 570 575  
 Tyr Ser Lys Asp Leu Gly Ile Tyr Val Pro Val Leu Asp Lys Glu Arg  
 580 585 590  
 Leu Phe Cys Ser Ala Ala Tyr Pro Lys Gly Val Glu Asn Lys Ser Leu  
 595 600 605  
 Lys Ser Lys Val Gly Ile Glu Gln Ala Tyr Lys Val Val Arg Tyr Glu  
 610 615 620  
 Ala Leu Arg Leu Val Gly Gly Trp Asn Tyr Pro Leu Leu Asn Lys Ala  
 625 630 635 640  
 Cys Lys Asn Asn Ala Ser Ala Ala Arg Arg His Leu Glu Ala Lys Gly  
 645 650 655  
 Phe Pro Leu Asp Glu Phe Leu Ala Glu Trp Ser Glu Leu Ser Glu Phe  
 660 665 670  
 Gly Glu Ala Phe Glu Gly Phe Asn Ile Lys Leu Thr Val Thr Pro Glu  
 675 680 685  
 Ser Leu Ala Glu Leu Asn Arg Pro Val Pro Pro Lys Pro Pro Asn Val  
 690 695 700  
 Asn Arg Pro Val Asn Thr Gly Gly Leu Lys Ala Val Ser Asn Ala Leu  
 705 710 715 720  
 Lys Thr Gly Arg Tyr Arg Asn Glu Ala Gly Leu Ser Gly Leu Val Leu  
 725 730 735  
 Leu Ala Thr Ala Arg Ser Arg Leu Gln Asp Ala Val Lys Ala Lys Ala  
 740 745 750  
 Glu Ala Glu Lys Leu His Lys Ser Lys Pro Asp Asp Pro Asp Ala Asp  
 755 760 765  
 Trp Phe Glu Arg Ser Glu Thr Leu Ser Asp Leu Leu Glu Lys Ala Asp  
 770 775 780  
 Ile Ala Ser Lys Val Ala His Ser Ala Leu Val Glu Thr Ser Asp Ala  
 785 790 795 800  
 Leu Glu Ala Val Gln Ser Thr Ser Val Tyr Thr Pro Lys Tyr Pro Glu  
 805 810 815  
 Val Lys Asn Pro Gln Thr Ala Ser Asn Pro Val Val Gly Leu His Leu

820                      825                      830  
 Pro Ala Lys Arg Ala Thr Gly Val Gln Ala Ala Leu Leu Gly Ala Gly  
           835                      840                      845  
 Thr Ser Arg Pro Met Gly Met Glu Ala Pro Thr Arg Ser Lys Asn Ala  
           850                      855                      860  
 Val Lys Met Ala Lys Arg Arg Gln Arg Gln Lys Glu Ser Arg Gln  
 865                      870                      875

<210> 84  
 <211> 145  
 <212> PRT  
 <213> Infectious bursal disease virus

<220>  
 <221> DOMAIN  
 <222> (1)..(145)  
 <223> Consensus sequence of IBDV VP5, ~~whereby the Xaa~~  
~~indicator may be any amino acid~~

<220>  
<221> MISC FEATURE  
<222> (14)  
<223> The 'Xaa' at position 14 may be any amino acid

<220>  
<221> MISC FEATURE  
<222> (45)  
<223> The 'Xaa' at position 45 may be any amino acid

<220>  
<221> MISC FEATURE  
<222> (74)  
<223> The 'Xaa' at position 74 may be any amino acid

<220>  
<221> MISC FEATURE  
<222> (125)  
<223> The 'Xaa' at position 125 may be any amino acid

<400> 84  
 Met Val Ser Arg Asp Gln Thr Asn Asp Arg Ser Asp Asp Xaa Pro Ala  
   1                          5                          10                          15  
 Arg Ser Asn Pro Thr Asp Cys Ser Val His Thr Glu Pro Ser Asp Ala  
           20                          25                          30  
 Asn Asn Arg Thr Gly Val His Ser Gly Arg His Pro Xaa Glu Ala His  
       35                          40                          45



Ser Gln Val Arg Asp Leu Asp Leu Gln Phe Asp Cys Gly Gly His Arg  
 50 55 60  
 Val Arg Ala Asn Cys Leu Phe Pro Trp Xaa Pro Trp Leu Asn Cys Gly  
 65 70 75 80  
 Cys Ser Leu His Thr Ala Glu Gln Trp Glu Leu Gln Val Arg Ser Asp  
 85 90 95  
 Ala Pro Asp Cys Pro Glu Pro Thr Gly Gln Leu Gln Leu Leu Gln Ala  
 100 105 110  
 Ser Glu Ser Glu Ser His Ser Glu Val Lys His Thr Xaa Trp Trp Arg  
 115 120 125  
 Leu Cys Thr Lys Xaa His His Lys Arg Arg Asp Leu Pro Arg Lys Pro  
 130 135 140  
 Glu  
 145

<210> 85  
 <211> 145  
 <212> PRT  
 <213> Infectious bursal disease virus

<220>  
 <221> DOMAIN  
 <222> (1)..(145)  
 <223> Sequence of IBDV D6948-VP5

<400> 85  
 Met Val Ser Arg Asp Gln Thr Asn Asp Arg Ser Asp Asp Glu Pro Ala  
 1 5 10 15  
 Arg Ser Asn Pro Thr Asp Cys Ser Val His Thr Glu Pro Ser Asp Ala  
 20 25 30  
 Asn Asn Arg Thr Gly Val His Ser Gly Arg His Pro Arg Glu Ala His  
 35 40 45  
 Ser Gln Val Arg Asp Leu Asp Leu Gln Phe Asp Cys Gly Gly His Arg  
 50 55 60  
 Val Arg Ala Asn Cys Leu Phe Pro Trp Phe Pro Trp Leu Asn Cys Gly  
 65 70 75 80  
 Cys Ser Leu His Thr Ala Glu Gln Trp Glu Leu Gln Val Arg Ser Asp  
 85 90 95  
 Ala Pro Asp Cys Pro Glu Pro Thr Gly Gln Leu Gln Leu Leu Gln Ala  
 100 105 110  
 Ser Glu Ser Glu Ser His Ser Glu Val Lys His Thr Pro Trp Trp Arg

115 120 125  
 Leu Cys Thr Lys Trp His His Lys Arg Arg Asp Leu Pro Arg Lys Pro  
 130 135 140

Glu  
 145

<210> 86  
 <211> 145  
 <212> PRT  
 <213> Infectious bursal disease virus

<220>  
 <221> DOMAIN  
 <222> (1)..(145)  
 <223> Sequence of IBDV CEF94-VP5

<400> 86  
 Met Val Ser Arg Asp Gln Thr Asn Asp Arg Ser Asp Asp Lys Pro Ala  
 1 5 10 15

Arg Ser Asn Pro Thr Asp Cys Ser Val His Thr Glu Pro Ser Asp Ala  
 20 25 30

Asn Asn Arg Thr Gly Val His Ser Gly Arg His Pro Gly Glu Ala His  
 35 40 45

Ser Gln Val Arg Asp Leu Asp Leu Gln Phe Asp Cys Gly Gly His Arg  
 50 55 60

Val Arg Ala Asn Cys Leu Phe Pro Trp Ile Pro Trp Leu Asn Cys Gly  
 65 70 75 80

Cys Ser Leu His Thr Ala Glu Gln Trp Glu Leu Gln Val Arg Ser Asp  
 85 90 95

Ala Pro Asp Cys Pro Glu Pro Thr Gly Gln Leu Gln Leu Leu Gln Ala  
 100 105 110

Ser Glu Ser Glu Ser His Ser Glu Val Lys His Thr Ser Trp Trp Arg  
 115 120 125

Leu Cys Thr Lys Arg His His Lys Arg Arg Asp Leu Pro Arg Lys Pro  
 130 135 140

Glu  
 145

<210> 87  
 <211> 149  
 <212> PRT  
 <213> Infectious bursal disease virus

<220>

<221> DOMAIN

<222> (1)..(149)

<223> Sequence of IBDV D6948-VP5

<400> 87

Met Leu Ser Leu Met Val Ser Arg Asp Gln Thr Asn Asp Arg Ser Asp  
1 5 10 15

Asp Glu Pro Ala Arg Ser Asn Pro Thr Asp Cys Ser Val His Thr Glu  
20 25 30

Pro Ser Asp Ala Asn Asn Arg Thr Gly Val His Ser Gly Arg His Pro  
35 40 45

Arg Glu Ala His Ser Gln Val Arg Asp Leu Asp Leu Gln Phe Asp Cys  
50 55 60

Gly Gly His Arg Val Arg Ala Asn Cys Leu Phe Pro Trp Phe Pro Trp  
65 70 75 80

Leu Asn Cys Gly Cys Ser Leu His Thr Ala Glu Gln Trp Glu Leu Gln  
85 90 95

Val Arg Ser Asp Ala Pro Asp Cys Pro Glu Pro Thr Gly Gln Leu Gln  
100 105 110

Leu Leu Gln Ala Ser Glu Ser Glu Ser His Ser Glu Val Lys His Thr  
115 120 125

Pro Trp Trp Arg Leu Cys Thr Lys Trp His His Lys Arg Arg Asp Leu  
130 135 140

Pro Arg Lys Pro Glu [—————]  
145